Package: RTCGAToolbox (via r-universe)

November 24, 2026

Type Package

Title A new tool for exporting TCGA Firehose data

Version 2.44.0

Description Managing data from large scale projects such as The Cancer Genome Atlas (TCGA) for further analysis is an important and time consuming step for research projects. Several efforts, such as Firehose project, make TCGA pre-processed data publicly available via web services and data portals but it requires managing, downloading and preparing the data for following steps. We developed an open source and extensible R based data client for Firehose pre-processed data and demonstrated its use with sample case studies. Results showed that RTCGAToolbox could improve data management for researchers who are interested with TCGA data. In addition, it can be integrated with other analysis pipelines for following data analysis.

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Depends R (>= 4.3.0)

Imports BiocGenerics, data.table, DelayedArray, GenomicRanges, Seqinfo, httr, methods, RaggedExperiment, RCurl, RJSONIO, rvest, S4Vectors, stats, stringr, SummarizedExperiment, TCGAutils, utils

Suggests BiocStyle, Homo.sapiens, knitr, readr, rmarkdown

biocViews DifferentialExpression, GeneExpression, Sequencing

URL http://mksamur.github.io/RTCGAToolbox/

BugReports https://github.com/mksamur/RTCGAToolbox/issues

VignetteBuilder knitr

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

Collate 'RTCGAToolbox-Class.R' 'RTCGAToolbox.R' 'utils.R' 'biocExtract.R' 'data.R' 'getBroadSubtypes.R' 'getFirehoseAnalyzeDates.R' 'getFirehoseData.R'

'getFirehoseDatasets.R' 'getFirehoseRunningDates.R'
'getGISTICPeaks.R' 'getLinks.R' 'getMutationRate.R'
'makeSummarizedExperimentFromGISTIC.R' 'selectType.R'

Encoding UTF-8

Date 2024-12-18

Config/pak/sysreqs make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:35:40 UTC

RemoteUrl https://github.com/bioc/RTCGAToolbox

RemoteRef RELEASE_3_24

RemoteSha f3043f16e976327573dd04f65053cec10451a6a1

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accmini *A subset of the Adrenocortical Carcinoma (ACC) dataset*

Description

See the acc_sample.R script to see how the data was generated. This dataset contains real data from the The Cancer Genome Atlas for the pipeline run date and GISTIC analysis date of 2016-01-28.

Usage

```
data("accmini", package = "RTCGAToolbox")
```

Format

A FirehoseData data object

biocExtract *Extract and convert data from a* FirehoseData *object to a* Bioconductor *object*

Description

This function processes data from a FirehoseData object. Raw data is converted to a conventional Bioconductor object. The function returns either SummarizedExperiment or RaggedExperiment. In cases where there are multiple platforms in a data type, an attempt to consolidate datasets will be made based on matching dimension names. For ranged data, this functionality is provided with more control as part of the RaggedExperiment features. See the RaggedExperiment-class for more details.

Usage

```
biocExtract(
  object,
  type = c("clinical", "RNASeqGene", "RNASeq2Gene", "miRNASeqGene", "RNASeq2GeneNorm",
   "CNASNP", "CNVSNP", "CNASeq", "CNACGH", "Methylation", "Mutation", "mRNAArray",
    "miRNAArray", "RPPAArray", "GISTIC", "GISTICA", "GISTICT", "GISTICP"),
  ...
)
```

Arguments

object	A FirehoseData object from which to extract data.
type	The type of data to extract from the "FirehoseData" object, see type section.
...	Additional arguments passed to lower level functions that convert tabular data into Bioconductor object such as .makeRangedSummarizedExperimentFromDataFrame or .makeRaggedExperimentFromDataFrame

Details

A typical additional argument for this function passed down to lower level functions is the `names.field` which indicates the row names in the data. By default, it is the "Hugo_Symbol" column in the internal code that converts `data.frames` to `SummarizedExperiment` representations (via the `.makeSummarizedExperimentFromD` internal function).

Value

Either SummarizedExperiment or RaggedExperiment.

type

Choices include the following:

- clinical: Get the clinical data slot
- RNASeqGene: RNASeqGene, RNASeq v1
- RNASeqGene: RNASeq2Gene, RNASeq v2
- RNASeq2GeneNorm: RNASeq v2 Normalized
- miRNASeqGene: micro RNA SeqGene
- CNASNP: Copy Number Alteration
- CNVSNP: Copy Number Alteration (germline CNVs removed)
- CNASeq: Copy Number Alteration
- CNACGH: Copy Number Alteration
- Methylation: Methylation
- mRNAArray: Messenger RNA
- miRNAArray: micro RNA
- RPPAArray: Reverse Phase Protein Array
- Mutation: Mutations
- GISTICA: GISTIC v2 ('AllByGene' only)
- GISTICT: GISTIC v2 ('ThresholdedByGene' only)
- GISTICP: GISTIC v2 ('Peaks' only)
- GISTIC: GISTIC v2 scores, probabilities, and peaks

Author(s)

Marcel Ramos <marcel.ramos@sph.cuny.edu>

Examples

```
data(accmini)
biocExtract(accmini, "RNASeq2Gene")
biocExtract(accmini, "miRNASeqGene")
biocExtract(accmini, "RNASeq2GeneNorm")
biocExtract(accmini, "CNASNP")
```

```
biocExtract(accmini, "CNVSNP")
biocExtract(accmini, "Methylation")
biocExtract(accmini, "Mutation")
biocExtract(accmini, "RPPAArray")
biocExtract(accmini, "GISTIC")
```

`CorResult-class` *An S4 class to store correlations between gene expression level and copy number data*

Description

An S4 class to store correlations between gene expression level and copy number data

Slots

`Dataset` A cohort name

`Correlations` Results data frame

`DGEResult-class` *An S4 class to store differential gene expression results*

Description

An S4 class to store differential gene expression results

Slots

`Dataset` Dataset name

`Toptable` Results data frame

`FirehoseCGHArray-class`
An S4 class to store data from CGA platforms

Description

An S4 class to store data from CGA platforms

Slots

`Filename` Platform name

`DataMatrix` A data frame that stores the CGH data.

`FirehoseData-class` *An S4 class to store main data object from clinent function.*

Description

An S4 class to store main data object from clinent function.

Usage

```
## S4 method for signature 'FirehoseData'
show(object)

## S4 method for signature 'FirehoseData'
getData(object, type, platform)

## S4 method for signature 'FirehoseGISTIC'
getData(object, type, platform)

## S4 method for signature 'ANY'
getData(object, type, platform)

## S4 method for signature 'FirehoseData'
updateObject(object, ..., verbose = FALSE)

## S4 method for signature 'FirehoseData'
selectType(object, dataType)
```

Arguments

`object`	A FirehoseData object
`type`	A data type to be extracted
`platform`	An index for data types that may come from multiple platforms (such as mRNAArray), for GISTIC data, one of the options: 'AllByGene', 'ThresholdedByGene', or 'Peaks'
`...`	additional arguments for updateObject
`verbose`	logical (default FALSE) whether to print extra messages
`dataType`	An available data type, see object show method

Methods (by generic)

- `show(FirehoseData)`: show method
- `getData(FirehoseData)`: Get a matrix or data.frame from `FirehoseData`
- `getData(FirehoseGISTIC)`: Get GISTIC data from `FirehoseData`
- `getData(ANY)`: Default method for getting data from `FirehoseData`

- `updateObject(FirehoseData)`: Update an old RTCGAToolbox FirehoseData object to the most recent API
- `selectType(FirehoseData)`: Extract data type

Slots

`Dataset` A cohort name

`runDate` Standard data run date from getFirehoseRunningDates

`gistic2Date` Analyze running date from getFirehoseAnalyzeDates

`clinical` clinical data frame

`RNASeqGene` Gene level expression data matrix from RNAseq

`RNASeq2Gene` Gene level expression data matrix from RNAseqV2

`RNASeq2GeneNorm` Gene level expression data matrix from RNAseqV2 (RSEM)

`miRNASeqGene` miRNA expression data from matrix smallRNAseq

`CNASNP` A data frame to store somatic copy number alterations from SNP array platform, not filtered for germline CNVs (`segmented_scna_hg19`)

`CNVSNP` A data frame to store somatic copy number alterations from SNP array platform with germline CNVs removed (`segmented_scna_minus_germline_cnv_hg19`)

`CNASeq` A data frame to store somatic copy number alterations from sequencing platform

`CNACGH` A list that stores `FirehoseCGHArray` object for somatic copy number alterations from CGH platform

`Methylation` A list that stores `FirehoseMethylationArray` object for methylation data

`mRNAArray` A list that stores `FirehosemRNAArray` object for gene expression data from microarray

`miRNAArray` A list that stores `FirehosemRNAArray` object for miRNA expression data from microarray

`RPPAArray` A list that stores `FirehosemRNAArray` object for RPPA data

`Mutation` A data frame for mutation infromation from sequencing data

`GISTIC` A `FirehoseGISTIC` object to store processed copy number data

`BarcodeUUID` A data frame that stores the Barcodes, UUIDs and Short sample identifiers

---

`FirehoseGISTIC-class` *An S4 class to store processed copy number data. (Data processed by using GISTIC2 algorithm)*

Description

An S4 class to store processed copy number data. (Data processed by using GISTIC2 algorithm)

Usage

```
## S4 method for signature 'FirehoseGISTIC'
isEmpty(x)

## S4 method for signature 'FirehoseGISTIC'
updateObject(object, ..., verbose = FALSE)
```

Arguments

x	A FirehoseGISTIC class object
object	A FirehoseGISTIC object
...	additional arguments for updateObject
verbose	logical (default FALSE) whether to print extra messages

Methods (by generic)

- isEmpty(FirehoseGISTIC): check whether the FirehoseGISTIC object has data in it or not
- updateObject(FirehoseGISTIC): Update an old FirehoseGISTIC object to the most recent API

Slots

Dataset Cohort name

AllByGene A data frame that stores continuous copy number

ThresholdedByGene A data frame for discrete copy number data

Peaks A data frame storing GISTIC peak data. See getGISTICPeaks.

FirehoseMethylationArray-class

An S4 class to store data from methylation platforms

Description

An S4 class to store data from methylation platforms

Slots

Filename Platform name

DataMatrix A data frame that stores the methylation data.

FirehosemRNAArray-class

An S4 class to store data from array (mRNA, miRNA etc.) platforms

Description

An S4 class to store data from array (mRNA, miRNA etc.) platforms

Slots

`Filename` Platform name

`DataMatrix` A data matrix that stores the expression data.

getBroadSubtypes

Download expression-based cancer subtypes from the Broad Institute

Description

Obtain the mRNA expression clustering results from the Broad Institute for a specific cancer code (see getFirehoseDatasets).

Usage

```
getBroadSubtypes(dataset, clust.alg = c("CNMF", "ConsensusPlus"))
```

Arguments

`dataset`	A TCGA cancer code, e.g. "OV" for ovarian cancer
`clust.alg`	The selected cluster algorithm, either "CNMF" or "ConsensusPlus" (default "CNMF")

Value

A `data.frame` of cluster and silhouette values

Author(s)

Ludwig Geistlinger

Examples

```
co <- getBroadSubtypes("COAD", "CNMF")
head(co)
```

getData *Extract data from FirehoseData object*

Description

A go-to function for getting top level information from a FirehoseData object. Available datatypes for a particular object can be seen by entering the object name in the console ('show' method).

Usage

```
getData(object, type, platform)
```

Arguments

object	A FirehoseData object
type	A data type to be extracted
platform	An index for data types that may come from multiple platforms (such as mRNAArray), for GISTIC data, one of the options: 'AllByGene' or 'ThresholdedByGene'

Value

Returns matrix or data.frame depending on data type

Examples

```
data(accmini)
getData(accmini, "clinical")
getData(accmini, "RNASeq2GeneNorm")
getData(accmini, "Methylation", 1)[1:4]
```

getFirehoseAnalyzeDates *Get data analyze dates.*

Description

`getFirehoseAnalyzeDates` returns the character vector for analyze release dates.

Usage

```
getFirehoseAnalyzeDates(last = NULL)
```

Arguments

last	To list last n dates. (Default NULL)

Value

A character vector for dates.

Examples

```
getFirehoseAnalyzeDates(last=2)
```

---

getFirehoseData *Get data from Firehose portal.*

Description

getFirehoseData returns FirehoseData object that stores TCGA data.

Usage

```
getFirehoseData(
  dataset,
  runDate = "20160128",
  gistic2Date = "20160128",
  RNASeqGene = FALSE,
  RNASeq2Gene = FALSE,
  clinical = TRUE,
  miRNASeqGene = FALSE,
 miRNASeqGeneType = c("read_count", "reads_per_million_miRNA_mapped", "cross-mapped"),
  RNASeq2GeneNorm = FALSE,
  CNASNP = FALSE,
  CNVSNP = FALSE,
  CNASeq = FALSE,
  CNACGH = FALSE,
  Methylation = FALSE,
  Mutation = FALSE,
  mRNAArray = FALSE,
  miRNAArray = FALSE,
  RPPAArray = FALSE,
  GISTIC = FALSE,
  RNAseqNorm = "raw_count",
  RNAseq2Norm = c("normalized_counts", "RSEM_normalized_log2", "raw_counts",
    "scaled_estimate"),
  forceDownload = FALSE,
  destdir = .setCache(),
  fileSizeLimit = 500,
  getUUIDs = FALSE,
```

```
  ...
)
```

Arguments

dataset	A cohort disease code. TCGA cancer codes can be obtained via getFirehoseDatasets
runDate	Standard data run dates. Date list can be accessible via getFirehoseRunningDates
gistic2Date	Analysis run date for GISTIC obtained via getFirehoseAnalyzeDates
RNASeqGene	Logical (default FALSE) RNAseq TPM data.
RNASeq2Gene	Logical (default FALSE) RNAseq v2 (RSEM processed) data; see RNAseqNorm argument.
clinical	Logical (default TRUE) clinical data.
miRNASeqGene	Logical (default FALSE) smallRNAseq data.
miRNASeqGeneType	Character (default "read_count") Indicate which type of data should be pulled from the miRNASeqGene data. Must be one of "reads_per_million_miRNA_mapped", "read_count", or "cross-mapped".
RNASeq2GeneNorm	Logical (default FALSE) RNAseq v2 (RSEM processed) data.
CNASNP	Logical (default FALSE) somatic copy number alterations data from SNP array, not filtered for germline CNVs (Firehose segmented_scna_hg19).
CNVSNP	Logical (default FALSE) somatic copy number alterations data from SNP array with germline CNVs removed (Firehose segmented_scna_minus_germline_cnv_hg19).
CNASeq	Logical (default FALSE) somatic copy number alterations data from sequencing.
CNACGH	Logical (default FALSE) somatic copy number alterations data from CGH.
Methylation	Logical (default FALSE) methylation data.
Mutation	Logical (default FALSE) mutation data from sequencing.
mRNAArray	Logical (default FALSE) mRNA expression data from microarray.
miRNAArray	Logical (default FALSE) miRNA expression data from microarray.
RPPAArray	Logical (default FALSE) RPPA data
GISTIC	logical (default FALSE) processed copy number data
RNAseqNorm	RNAseq data normalization method. (Default raw_count)
RNAseq2Norm	RNAseq v2 data normalization method. (Default normalized_count or one of RSEM_normalized_log2, raw_count, scaled_estimate)
forceDownload	A logic (Default FALSE) key to force download RTCGAToolbox every time. By default if you download files into your working directory once than RTCGAToolbox using local files next time.
destdir	Directory in which to store the resulting downloaded file. Defaults to a cache directory given by RTCGAToolbox:::.setCache().

fileSizeLimit	Files that are larger than set value (megabyte) won't be downloaded (Default: 500)
getUUIDs	Logical key to get UUIDs from barcode (Default: FALSE)
...	Additional arguments to pass down.

Details

This is a main client function to download data from Firehose TCGA portal.

To avoid unnecessary downloads, we use `tools::R_user_dir("RTCGAToolbox", "cache")` to set the default `destdir` parameter to the cached directory. To get the actual default directory, one can run `RTCGAToolbox:::.setCache()`.

Value

A `FirehoseData` data object that stores data for selected data types.

See Also

getLinks, https://gdac.broadinstitute.org/

Examples

```
# Sample Dataset
data(accmini)
accmini
## Not run:
BRCAdata <- getFirehoseData(dataset="BRCA",
runDate="20140416",gistic2Date="20140115",
RNASeqGene=TRUE,clinical=TRUE,mRNAArray=TRUE,Mutation=TRUE)

## End(Not run)
```

---

getFirehoseDatasets *Get a list of TCGA disease cohorts*

Description

`getFirehoseDatasets` returns a character vector of TCGA disease codes. A reference table can be seen at https://gdac.broadinstitute.org/.

Usage

```
getFirehoseDatasets()
```

Value

A character string

See Also

https://gdac.broadinstitute.org/

Examples

```
getFirehoseDatasets()
```

`getFirehoseRunningDates` *Get standard data running dates.*

Description

`getFirehoseRunningDates` returns the character vector for standard data release dates.

Usage

```
getFirehoseRunningDates(last = NULL)
```

Arguments

`last`	To list last n dates. (Default NULL)

Value

A character vector for dates.

Examples

```
getFirehoseRunningDates()
getFirehoseRunningDates(last=2)
```

`getGISTICPeaks` *Download GISTIC2 peak-level data from the Firehose pipeline*

Description

Access GISTIC2 level 4 copy number data through `gdac.broadinstitute.org`

Usage

```
getGISTICPeaks(object, peak = c("wide", "narrow", "full"), rm.chrX = TRUE)
```

Arguments

object	A FirehoseData GISTIC type object
peak	The peak type, select from "wide", "narrow", "full".
rm.chrX	(logical default TRUE) Whether to remove observations in the X chromosome

Value

A data.frame of peak values

Author(s)

Ludwig Geistlinger

Examples

```
co <- getFirehoseData("COAD", clinical = FALSE, GISTIC = TRUE)
peaks <- getGISTICPeaks(co, "wide")
class(peaks)
head(peaks)[1:6]
```

---

getLinks *Get resource links from inputs*

Description

This function provides a reference to the resources downloaded from the GDAC Firehose pipeline. Based on the input, the function returns a URL location to the resource if there exists one.

Usage

```
getLinks(
  dataset,
  data_date = "20160128",
  RNASeqGene = FALSE,
  RNASeq2Gene = FALSE,
  clinical = FALSE,
  miRNASeqGene = FALSE,
  RNASeq2GeneNorm = FALSE,
  RNAseq2Norm = c("normalized_counts", "RSEM_normalized_log2", "raw_counts",
    "scaled_estimate"),
  CNASNP = FALSE,
  CNVSNP = FALSE,
  CNASeq = FALSE,
  CNACGH = FALSE,
  Methylation = FALSE,
  Mutation = FALSE,
```

```
  mRNAArray = FALSE,
  miRNAArray = FALSE,
  RPPAArray = FALSE,
  GISTIC = FALSE
)
```

Arguments

dataset	A cohort disease code. TCGA cancer codes can be obtained via getFirehoseDatasets
data_date	Either a runDate or analysisDate typically entered in getFirehoseData
RNASeqGene	Logical (default FALSE) RNAseq TPM data.
RNASeq2Gene	Logical (default FALSE) RNAseq v2 (RSEM processed) data; see RNAseqNorm argument.
clinical	Logical (default TRUE) clinical data.
miRNASeqGene	Logical (default FALSE) smallRNAseq data.
RNASeq2GeneNorm	Logical (default FALSE) RNAseq v2 (RSEM processed) data.
RNAseq2Norm	RNAseq v2 data normalization method. (Default normalized_count or one of RSEM_normalized_log2, raw_count, scaled_estimate)
CNASNP	Logical (default FALSE) somatic copy number alterations data from SNP array, not filtered for germline CNVs (Firehose segmented_scna_hg19).
CNVSNP	Logical (default FALSE) somatic copy number alterations data from SNP array with germline CNVs removed (Firehose segmented_scna_minus_germline_cnv_hg19).
CNASeq	Logical (default FALSE) somatic copy number alterations data from sequencing.
CNACGH	Logical (default FALSE) somatic copy number alterations data from CGH.
Methylation	Logical (default FALSE) methylation data.
Mutation	Logical (default FALSE) mutation data from sequencing.
mRNAArray	Logical (default FALSE) mRNA expression data from microarray.
miRNAArray	Logical (default FALSE) miRNA expression data from microarray.
RPPAArray	Logical (default FALSE) RPPA data
GISTIC	logical (default FALSE) processed copy number data

Value

A character URL to a dataset location

Examples

```
getLinks("BRCA", CNASeq = TRUE)
```

getMutationRate *Make a table for mutation rate of each gene in the cohort*

Description

Make a table for mutation rate of each gene in the cohort

Usage

```
getMutationRate(dataObject)
```

Arguments

dataObject	This must be FirehoseData object.

Value

Returns a data table

Examples

```
data(accmini)
mutRate <- getMutationRate(dataObject=accmini)
mutRate <- mutRate[order(mutRate[,2],decreasing = TRUE),]
head(mutRate)
```

hg19.ucsc.gene.locations *Gene coordinates for circle plot.*

Description

A dataset containing the gene coordinates The variables are as follows:

Format

A data frame with 28454 rows and 5 variables

Details

- GeneSymbol: Gene symbols
- Chromosome: Chromosome name
- Strand: Gene strand on chromosome
- Start: Gene location on chromosome
- End: Gene location on chromosome

makeSummarizedExperimentFromGISTIC
Create a SummarizedExperiment from FireHose GISTIC

Description

Use the output of `getFirehoseData` to create a SummarizedExperiment. This can be done for three types of data, G-scores threshold by gene, copy number by gene, and copy number by peak regions.

Usage

```
makeSummarizedExperimentFromGISTIC(
  gistic,
  dataType = c("AllByGene", "ThresholdedByGene", "Peaks"),
  rownameCol = "Gene.Symbol",
  ...
)
```

Arguments

`gistic`	A FirehoseGISTIC object
`dataType`	character(1) One of "ThresholdedByGene" (default), "AllByGene", or "Peaks"
`rownameCol`	character(1) The name of the column in the data to use as rownames in the data matrix (default: 'Gene.Symbol'). The row names are only set when the column name is found in the data and all values are unique.
`...`	Additional arguments passed to 'getGISTICPeaks'.

Value

A `SummarizedExperiment` object

Author(s)

L. Geistlinger, M. Ramos

Examples

```
co <- getFirehoseData("COAD", clinical = FALSE, GISTIC = TRUE,
    destdir = tempdir())
makeSummarizedExperimentFromGISTIC(co, "AllByGene")
```

RTCGAToolbox *RTCGAToolbox: A New Tool for Exporting TCGA Firehose Data*

Description

Managing data from large-scale projects (such as The Cancer Genome Atlas (TCGA) for further analysis is an important and time consuming step for research projects. Several efforts, such as the Firehose project, make TCGA pre-processed data publicly available via web services and data portals, but this information must be managed, downloaded and prepared for subsequent steps. We have developed an open source and extensible R based data client for pre-processed data from the Firehose, and demonstrate its use with sample case studies. Results show that our RTCGAToolbox can facilitate data management for researchers interested in working with TCGA data. The RTCGAToolbox can also be integrated with other analysis pipelines for further data processing.

Details

The main function you're likely to need from `RTCGAToolbox` is getFirehoseData. Otherwise refer to the vignettes to see how to use the `RTCGAToolbox`

Author(s)

Mehmet Kemal Samur

See Also

Useful links:

- http://mksamur.github.io/RTCGAToolbox/
- Report bugs at https://github.com/mksamur/RTCGAToolbox/issues

---

`selectType` *Accessor function for the FirehoseData object*

Description

An accessor function for the FirehoseData. An argument will specify the data type to return See FirehoseData for more details.

Usage

```
selectType(object, dataType)
```

Arguments

`object`	A `FirehoseData` class object
`dataType`	A data type, see details.

Details

- clinical: Get the clinical data slot
- RNASeqGene: RNASeqGene
- RNASeq2GeneNorm: Normalized
- miRNASeqGene: micro RNA SeqGene
- CNASNP: Copy Number Alteration
- CNVSNP: Copy Number Alteration (germline CNVs removed)
- CNASeq: Copy Number Alteration
- CNACGH: Copy Number Alteration
- Methylation: Methylation
- mRNAArray: Messenger RNA
- miRNAArray: micro RNA
- RPPAArray: Reverse Phase Protein Array
- Mutation: Mutations
- GISTIC: GISTIC v2 scores and probabilities

Value

The data type element of the `FirehoseData` object

`showResults` *Export toptable or correlation data frame*

Description

Export toptable or correlation data frame

Usage

```
showResults(object)
```

Arguments

`object`	A DGEResult or CorResult object

Value

Returns toptable or correlation data frame

Examples

```
data(accmini)
```

showResults,CorResult-method
Export toptable or correlation data frame

Description

Export toptable or correlation data frame

Usage

```
## S4 method for signature 'CorResult'
showResults(object)
```

Arguments

object	A DGEResult or CorResult object

Value

Returns correlation results data frame

Examples

```
data(accmini)
```

showResults,DGEResult-method
Export toptable or correlation data frame

Description

Export toptable or correlation data frame

Usage

```
## S4 method for signature 'DGEResult'
showResults(object)
```

Arguments

object	A DGEResult or CorResult object

Value

Returns toptable for DGE results

Examples

```
data(accmini)
```

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